

-continued

<400> SEQUENCE: 480

```

Tyr Thr Ser Asn Glu Pro Val Met Leu Cys Leu Met Ser Ala Ile Glu
1           5           10           15

Thr Gly Val Ile Phe Leu Ile Asn Asp Gly Ile Asp Arg Gly Leu Trp
          20           25           30

Asp Leu Gln Asn Lys Ala Glu Arg Gln Asn Asp Ile Leu Val Lys Tyr
          35           40           45

Arg His Met Ser Val Pro Pro Glu Ser
          50           55

```

<210> SEQ ID NO 481

<211> LENGTH: 56

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 481

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Tyr Thr Asn Asn Glu Pro Val Asn Val Ala Val Met Ser Ala Ile Asp
1           5           10           15

Ala Ala Val Ile His Leu Ile Val Lys Gly Ile Gly Arg Gly Leu Trp
          20           25           30

Gln Pro Glu Asn Lys Glu Asp Leu Gln Asp Glu Thr Ile Gln Arg Tyr
          35           40           45

Ala Lys Gln Thr His Gln Ile Leu
          50           55

```

<210> SEQ ID NO 482

<211> LENGTH: 66

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic polypeptide

<400> SEQUENCE: 482

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Tyr Thr Ser Asn Glu Pro Val Ser Leu Cys Val Ala Gln Ala Ile Glu
1           5           10           15

Ser Ala Val Val His Met Ile Ala Asp Gly Ile Trp Lys Arg Ala Trp
          20           25           30

Asn Leu Ala Asp Ser Gln Thr Gly Leu Glu Asn Pro Ile Leu Lys Lys
          35           40           45

Tyr Trp Leu Glu Ala His Ser Val Glu Arg Val Gln Ala Arg Leu Glu
          50           55           60

Gln Gly
          65

```

1.-76. (canceled)

77. A method for determining the presence, absence or one or more characteristics of a target analyte, comprising:

- (a) contacting the target analyte with a transmembrane pore comprising at least one CsgG monomer such that the target analyte moves with respect to the pore; and
- (b) taking one or more measurements as the analyte moves with respect to the pore and thereby determining the presence, absence or one or more characteristics of the analyte.

78. The method of claim 77, wherein the at least one CsgG monomer is a variant of SEQ ID NO: 390, said variant comprising: (a) mutations at one or more of the following positions N40, Q42, D43, E44, K49, Y51, S54, N55, F56, S57, Q62, E101, N102, E124, E131, R142, D149, T150, E185, R192, D195, E201 and E203; and/or (b) deletion of one or more of the following positions F48, K49, P50, Y51, P52, A53, S54, N55, F56 and S57. **[text missing or illegible when filed]** A method according to claim 95, wherein the variant comprises one or more of the following substitutions: (a) F56N, F56Q, F56R, F56S, F56G, F56A or F56K or F56A, F56P, F56R, F56H, F56S, F56Q, F56I,